

SEQUENCE LISTING

<110> ADVANCED RESEARCH AND TECHNOLOGY INSTITUTE, INC.
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CATT, DIANA M

<120> METHODS AND COMPOSITIONS FOR PROMOTING ORAL HEALTH, AND
POLYPEPTIDES USEFUL FOR SAME

<130> IU-104

<150> 10/009,004
<151> 2001-11-05

<150> 60/132,312
<151> 1999-05-03

<150> PCT/US00/11992
<151> 2000-05-03

<160> 8

<170> PatentIn version 3.3

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<213> Streptococcus mutans

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<212> DNA
<213> Streptococcus mutans

IU-104.ST25:o:kag:patentin3.3

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aat tta ccg gca caa gga acc tat cac ttt act aaa cag cag agc tta Asn Leu Pro Ala Gln Gly Thr Tyr His Phe Thr Lys Gln Gln Ser Leu 295 300 305 310	1025
aaa atg aag cta aac tgt cta gtc cga ccc aat tct cgt ttt aca acg Lys Met Lys Leu Asn Cys Leu Val Arg Pro Asn Ser Arg Phe Thr Thr 315 320 325	1073
gag atc acg ttt ttt atg ata agg ttt tag aagcgatgg acatcaatgg Glu Ile Thr Phe Phe Met Ile Arg Phe 330 335	1123
atttagctatg tgtcctacag tggtatccgt cgttatgtt ttattggaaa gcttacgaca caaccctctc caattgaaac taaagtatca ggtactattt tcattccaaaa taaaacggct caacaattcg atgttgtcat ttctaattgtc tcaagcaatc aaggcataaa agaggtatta gtgccagttt ggtcagagca aaacgggcag gatgacattt tctggatca agcaatcaa caaggtgaag gcgtttataa ggtgaccgtt aaggtcagtg accataaaaa taatagcggt aactatcatg tccatctttt ttatctttt gataatgggt aacaaagagg agtcggggca acaatgactg aggttgaagc accagagcct gtagaaacaa caggtatcat tagcattgcc aataagagca gccaggatt tgatgtttt attactaatg cttccagcac tcaagacata aaagaggttt tagtgcgggt ttggtcagaa caaaacggac aggacgatat tatttggat caagcaacta aacaaggcga aggctttt aaggtggccg ttaaggtcag tgaccataaa aatgacagtg gtaactataa cattcacctt tattatcgcc ttgttaactgg tgaattaaag gttggtagg gaaagacaac gacagtagaa gcccctaata gagcaatctt ccagcacaag gaacttatgt tttcactaat aaagttgagg ttaaaaatga ggccagaaca tctagtccaa ctcagtttac cttaataaaa ggagaaagta ttactatga cagtatctt aatgctgatg gacatcaatg gattagctat cgttcctaca gtggatttcg tcgttatatt atcattggtt ga	1183 1243 1303 1363 1423 1483 1543 1603 1663 1723 1783 1843 1903 1963 2023 2025

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His Ser Phe Ser Lys Ala Val Tyr His Asn Asp Arg Ser Val Lys Leu
20 25 30

Met Lys Arg Ile Asp Ile Asn His Gln Ala Gln Arg Phe Ser Ile Arg
35 40 45

Lys Tyr Ala Phe Gly Ala Ala Ser Val Leu Ile Gly Cys Val Phe Phe
50 55 60

Leu Gly Thr Gln Asn Val Ser Ala Gln Glu Gln Gly Thr Gln Leu Pro
65 70 75 80

Ala Ser Glu Asn Ala Val Val Asn Val Ala Glu Asn Ser Val Ala Ile
85 90 95

Ser Gln Ala Val Ala Asp Lys Ala Ala Thr Gln Thr Thr Leu Thr Glu
 100 105 110

Thr Pro Gln Val Glu Val Glu Glu Lys Glu Ser Lys Val Asn Ala Pro
 115 120 125

Ala Leu Asn Val Asp Asp Lys Gly Ala Lys Ser Lys Glu Asp Val Asn
 130 135 140

Pro Thr Ile Ser Lys Thr Ala Ser Glu Val Glu Ala Ser Ala Val Thr
 145 150 155 160

Ala Thr Asp Thr Lys Asn Ser Asn Pro Gln Val Asn Val Glu Thr Asp
 165 170 175

Ser Ser Glu Lys Asp Glu Asn Lys Met Val Thr Ser Ala Pro Ala Lys
 180 185 190

Glu Thr Glu Ala Glu Gln Asn Glu Lys Ala Val Arg Glu Asn Leu Met
 195 200 205

Gln Arg Gln Ala Lys Ala Val Ser Ile Pro Ser Gln Gly Asn Tyr Val
 210 215 220

Phe Gln Glu Thr Thr Pro Val Lys Asn Ala Ala Ser Met Ser Ser Pro
 225 230 235 240

Thr Gln Phe Asn Phe Asp Lys Gly Asp Lys Val Phe Tyr Asp Asn Val
 245 250 255

Leu Glu Ala Asp Gly His Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly
 260 265 270

Ile Arg Arg Tyr Ala Pro Ile Ala Val Thr Ile Glu Glu Leu Lys Gln
 275 280 285

Lys Glu Ile Val Gln Gln Asn Leu Pro Ala Gln Gly Thr Tyr His Phe
 290 295 300

Thr Lys Gln Gln Ser Leu Lys Met Lys Leu Asn Cys Leu Val Arg Pro
 305 310 315 320

Asn Ser Arg Phe Thr Thr Glu Ile Thr Phe Phe Met Ile Arg Phe
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aaa tat gca ttt gga gct gca tct gtt tta att ggc tgt gtc ttt ttt 96
 Lys Tyr Ala Phe Gly Ala Ala Ser Val Leu Ile Gly Cys Val Phe Phe

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20

25

30

ctt ggt acc caa aat gtt tct gca caa gag cag gga act caa ttg cca Leu Gly Thr Gln Asn Val Ser Ala Gln Glu Gln Gly Thr Gin Leu Pro 35 40 45	144
gca agt gaa aac gca gtt gtg aac gtg gct gaa aat tca gtt gct atc Ala Ser Glu Asn Ala Val Val Asn Val Ala Glu Asn Ser Val Ala Ile 50 55 60	192
agc caa gca gtt tca gat aag gca gca gct caa aca act cta aca gaa Ser Gln Ala Val Ser Asp Lys Ala Ala Gln Thr Thr Leu Thr Glu 65 70 75 80	240
aca ccc caa gtt gaa gtt gag gag aaa gaa aat aag gta aat gct cct Thr Pro Gln Val Glu Val Glu Lys Glu Asn Lys Val Asn Ala Pro 85 90 95	288
gct tta aat gtc gat gac aaa ggt gca aaa tcc aaa gaa gat gtg aac Ala Leu Asn Val Asp Asp Lys Gly Ala Lys Ser Lys Glu Asp Val Asn 100 105 110	336
cct act gtt tca aag aca gca agt gaa gtg gaa gct tct gca gta act Pro Thr Val Ser Lys Thr Ala Ser Glu Val Glu Ala Ser Ala Val Thr 115 120 125	384
gct act gat act aaa aat tca aat cca caa gtc aat gtt gaa act gac Ala Thr Asp Thr Lys Asn Ser Asn Pro Gln Val Asn Val Glu Thr Asp 130 135 140	432
tca aat gaa aaa gac gaa aat aaa atg gtc acc tcg gct cca gct aag Ser Asn Glu Lys Asp Glu Asn Lys Met Val Thr Ser Ala Pro Ala Lys 145 150 155 160	480
gag act gag gca gaa caa aat gag aaa gcg gta gca gaa aat ctt atg Glu Thr Glu Ala Glu Gln Asn Glu Lys Ala Val Ala Glu Asn Leu Met 165 170 175	528
caa aga caa gct aag gct gtc tca att cca tcg caa ggc aat tat gtt Gln Arg Gln Ala Lys Ala Val Ser Ile Pro Ser Gln Gly Asn Tyr Val 180 185 190	576
tcc caa gaa aca act cct gta aaa aat gca gcc agt atg tcc agc cca Phe Gln Glu Thr Thr Pro Val Lys Asn Ala Ala Ser Met Ser Ser Pro 195 200 205	624
acc caa ttt aac ttt gat aaa gga gat aag gtt ttt tat gat aag gtt Thr Gln Phe Asn Phe Asp Lys Gly Asp Lys Val Phe Tyr Asp Lys Val 210 215 220	672
tta gaa gcg gat ggg cat caa tgg att agc tat gtg tct tac agt ggt Leu Glu Ala Asp Gly His Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly 225 230 235 240	720
att cgt cgc tat gct cct att gct gtg aca att gaa gaa ttg aag caa Ile Arg Arg Tyr Ala Pro Ile Ala Val Thr Ile Glu Glu Leu Lys Gln 245 250 255	768
aaa gaa att gtt cag caa aat tta ccg gca caa gga acc tat cac ttt Lys Glu Ile Val Gln Gln Asn Leu Pro Ala Gln Gly Thr Tyr His Phe 260 265 270	816
act aaa caa gca gac gtt aaa aat gaa gct aaa ctg tct agt ccg acc Thr Lys Gln Ala Asp Val Lys Asn Glu Ala Lys Leu Ser Ser Pro Thr 275 280 285	864
caa ttc tcg ttt tac aac gga gat cac gtt ttt tat gat aag gtt tta Gln Phe Ser Phe Tyr Asn Gly Asp His Val Phe Tyr Asp Lys Val Leu 290 295 300	912
gaa gcg gat ggg cat caa tgg att agc tat gtg tcc tac agt ggt atc Glu Ala Asp Gly His Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly Ile 305 310 315 320	960
cgt cgt tat gtt gtt att gga aag ctt acg aca caa ccc tct cca att Arg Arg Tyr Val Val Ile Gly Lys Leu Thr Thr Gln Pro Ser Pro Ile 325 330 335	1008
gaa act aaa gta tca ggt act att gcc atc caa aat aaa acg gct caa	1056

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Glu Thr Lys Val Ser Gly Thr Ile Ala Ile Gln Asn Lys Thr Ala Gln			
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caa ttc gat gtt atc att tct aat gtt tcc agc act caa ggc ata aaa	1104		
Gln Phe Asp Val Ile Ile Ser Asn Val Ser Ser Thr Gln Gly Ile Lys			
355	360	365	
gag gta tta gtg ccg gtt tgg tca gag caa aac ggg cag gat gac att	1152		
Glu Val Leu Val Pro Val Trp Ser Glu Gln Asn Gly Gln Asp Asp Ile			
370	375	380	
gtc tgg tat caa gca act aaa caa ggc gaa ggc gtt tat aag gtg acc	1200		
Val Trp Tyr Gln Ala Thr Lys Gln Gly Glu Gly Val Tyr Lys Val Thr			
385	390	395	400
gtt aag gtc agt gac cat aaa aat aac agt ggt aac tat gac att cac	1248		
Val Lys Val Ser Asp His Lys Asn Asn Ser Gly Asn Tyr Asp Ile His			
405	410	415	
ctt tat tat cgc ctt tca act ggt gaa tta aag gtt gtt gga gga aag	1296		
Leu Tyr Tyr Arg Leu Ser Thr Gln Glu Leu Lys Val Val Gln Gly Lys			
420	425	430	
aca act gag gtg gaa gca ccg aag cct gta gaa aca aca ggt atc att	1344		
Thr Thr Glu Val Glu Ala Pro Lys Pro Val Glu Thr Thr Gly Ile Ile			
435	440	445	
agc att gcc aat aag agc agc caa gga ttt gat gtt ttg att act aat	1392		
Ser Ile Ala Asn Lys Ser Ser Gln Gly Phe Asp Val Leu Ile Thr Asn			
450	455	460	
gct tcc agc act caa ggc ata aaa gag gta tta gtg cca gtt tgg tca	1440		
Ala Ser Ser Thr Gln Gly Ile Lys Glu Val Leu Val Pro Val Trp Ser			
465	470	475	480
gaa caa aac gga cag gac gat att att tgg tat caa gca act aaa caa	1488		
Glu Gln Asn Gly Gln Asp Asp Ile Ile Trp Tyr Gln Ala Thr Lys Gln			
485	490	495	
ggc gaa ggc gtt tat aag gtg acc gtt aag gtc agt gac cat aaa aat	1536		
Gly Glu Gly Val Tyr Lys Val Thr Val Lys Val Ser Asp His Lys Asn			
500	505	510	
gac agt ggt aac tat gac att cac ctt tat tat cgc ctt tca act ggt	1584		
Asp Ser Gly Asn Tyr Asp Ile His Leu Tyr Tyr Arg Leu Ser Thr Gly			
515	520	525	
gaa tta aag gtt gtt gga gga aag aca acg aca gta gaa gcc cct aat	1632		
Glu Leu Lys Val Val Gly Gly Lys Thr Thr Thr Val Glu Ala Pro Asn			
530	535	540	
aga gtc aat ctt cca gca caa gga act tat gtt ttc act aat aaa gtt	1680		
Arg Val Asn Leu Pro Ala Gln Gly Thr Tyr Val Phe Thr Asn Lys Val			
545	550	555	560
gag gtt aaa aat gag gcc aga aca tct agt cca act cag ttt acc ttt	1728		
Glu Val Lys Asn Glu Ala Arg Thr Ser Ser Pro Thr Gln Phe Thr Phe			
565	570	575	
aat aaa gga gaa agt att tac tat gac agt atc ttg aat gct gat gga	1776		
Asn Lys Gly Glu Ser Ile Tyr Tyr Asp Ser Ile Leu Asn Ala Asp Gly			
580	585	590	
cat caa tgg att agc tat cgt tcc tac agt ggt att cgt cgt tat att	1824		
His Gln Trp Ile Ser Tyr Arg Ser Tyr Ser Gln Ile Arg Arg Tyr Ile			
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atc att gat tga	1836		
Ile Ile Asp			
610			

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Lys Tyr Ala Phe Gly Ala Ala Ser Val Leu Ile Gly Cys Val Phe Phe
20 25 30

Leu Gly Thr Gln Asn Val Ser Ala Gln Glu Gln Gly Thr Gln Leu Pro
35 40 45

Ala Ser Glu Asn Ala Val Val Asn Val Ala Glu Asn Ser Val Ala Ile
50 55 60

Ser Gln Ala Val Ser Asp Lys Ala Ala Gln Thr Thr Leu Thr Glu
65 70 75 80

Thr Pro Gln Val Glu Val Glu Glu Lys Glu Asn Lys Val Asn Ala Pro
85 90 95

Ala Leu Asn Val Asp Asp Lys Gly Ala Lys Ser Lys Glu Asp Val Asn
100 105 110

Pro Thr Val Ser Lys Thr Ala Ser Glu Val Glu Ala Ser Ala Val Thr
115 120 125

Ala Thr Asp Thr Lys Asn Ser Asn Pro Gln Val Asn Val Glu Thr Asp
130 135 140

Ser Asn Glu Lys Asp Glu Asn Lys Met Val Thr Ser Ala Pro Ala Lys
145 150 155 160

Glu Thr Glu Ala Glu Gln Asn Glu Lys Ala Val Ala Glu Asn Leu Met
165 170 175

Gln Arg Gln Ala Lys Ala Val Ser Ile Pro Ser Gln Gly Asn Tyr Val
180 185 190

Phe Gln Glu Thr Thr Pro Val Lys Asn Ala Ala Ser Met Ser Ser Pro
195 200 205

Thr Gln Phe Asn Phe Asp Lys Gly Asp Lys Val Phe Tyr Asp Lys Val
210 215 220

Leu Glu Ala Asp Gly His Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly
225 230 235 240

Ile Arg Arg Tyr Ala Pro Ile Ala Val Thr Ile Glu Glu Leu Lys Gln
245 250 255

Lys Glu Ile Val Gln Gln Asn Leu Pro Ala Gln Gly Thr Tyr His Phe
260 265 270

Thr Lys Gln Ala Asp Val Lys Asn Glu Ala Lys Leu Ser Ser Pro Thr
275 280 285

Gln Phe Ser Phe Tyr Asn Gly Asp His Val Phe Tyr Asp Lys Val Leu
290 295 300

Glu Ala Asp Gly His Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly Ile
305 310 315 320

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Arg Arg Tyr Val Val Ile Gly Lys Leu Thr Thr Gln Pro Ser Pro Ile
325 330 335

Glu Thr Lys Val Ser Gly Thr Ile Ala Ile Gln Asn Lys Thr Ala Gln
340 345 350

Gln Phe Asp Val Ile Ile Ser Asn Val Ser Ser Thr Gln Gly Ile Lys
355 360 365

Glu Val Leu Val Pro Val Trp Ser Glu Gln Asn Gly Gln Asp Asp Ile
370 375 380

Val Trp Tyr Gln Ala Thr Lys Gln Gly Glu Gly Val Tyr Lys Val Thr
385 390 395 400

Val Lys Val Ser Asp His Lys Asn Asn Ser Gly Asn Tyr Asp Ile His
405 410 415

Leu Tyr Tyr Arg Leu Ser Thr Gly Glu Leu Lys Val Val Gly Gly Lys
420 425 430

Thr Thr Glu Val Glu Ala Pro Lys Pro Val Glu Thr Thr Gly Ile Ile
435 440 445

Ser Ile Ala Asn Lys Ser Ser Gln Gly Phe Asp Val Leu Ile Thr Asn
450 455 460

Ala Ser Ser Thr Gln Gly Ile Lys Glu Val Leu Val Pro Val Trp Ser
465 470 475 480

Glu Gln Asn Gly Gln Asp Asp Ile Ile Trp Tyr Gln Ala Thr Lys Gln
485 490 495

Gly Glu Gly Val Tyr Lys Val Thr Val Lys Val Ser Asp His Lys Asn
500 505 510

Asp Ser Gly Asn Tyr Asp Ile His Leu Tyr Tyr Arg Leu Ser Thr Gly
515 520 525

Glu Leu Lys Val Val Gly Gly Lys Thr Thr Thr Val Glu Ala Pro Asn
530 535 540

Arg Val Asn Leu Pro Ala Gln Gly Thr Tyr Val Phe Thr Asn Lys Val
545 550 555 560

Glu Val Lys Asn Glu Ala Arg Thr Ser Ser Pro Thr Gln Phe Thr Phe
565 570 575

Asn Lys Gly Glu Ser Ile Tyr Tyr Asp Ser Ile Leu Asn Ala Asp Gly
580 585 590

His Gln Trp Ile Ser Tyr Arg Ser Tyr Ser Gly Ile Arg Arg Tyr Ile
595 600 605

Ile Ile Asp
610